



IFWO

RAW SEQUENCE LISTING DATE: 08/20/2004
 PATENT APPLICATION: US/10/764,330 TIME: 10:46:02

Input Set : A:\SEQ.Listing.ST25.txt.txt
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3 <110> APPLICANT: Cooke, Michael P.
 4 Sauer, Karsten
 5 Wiltshire, Tim
 6 Tarantino, Lisa
 7 Fletcher, Colin
 8 Wen, Ben
 10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES
 12 <130> FILE REFERENCE: P1097US10
 14 <140> CURRENT APPLICATION NUMBER: US 10/764,330
 15 <141> CURRENT FILING DATE: 2004-01-23
 17 <150> PRIOR APPLICATION NUMBER: US 60/442,792
 18 <151> PRIOR FILING DATE: 2003-01-25
 20 <160> NUMBER OF SEQ ID NOS: 4
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1192
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Mus musculus
 29 <400> SEQUENCE: 1
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 35 Ser Arg Glu Ile Val Tyr Gly Ala Trp Gly Gly Gly Arg Ala Arg Asp
 36 20 25 30
 39 Phe Ala Leu Cys Pro Pro Pro Arg Pro Cys Cys Ser Ile Ser Ala Gln
 40 35 40 45
 43 Ser Tyr Gly Arg Arg Ala Ser Gly Thr Lys Pro Arg Ala Ala Gly Gly
 44 50 55 60
 47 Gly Gly Ala Gly Gly Ala Gly Arg Arg Ala Ala Ala Ala Gly Gly
 48 65 70 75 80
 51 Pro Cys Thr Met Ala Val Tyr Cys Tyr Ala Leu Asn Ser Leu Val Ile
 52 85 90 95
 55 Met Asn Ser Thr Asn Glu Leu Lys Ser Gly Gly Pro Arg Pro Ser Gly
 56 100 105 110
 59 Ser Glu Thr Pro Gln Pro Ser Gly Arg Ala Ala Leu Ser Pro Gly Ser
 60 115 120 125
 63 Val Phe Ser Pro Gly Arg Gly Ala Ser Phe Leu Phe Pro Pro Ala Glu
 64 130 135 140
 67 Ser Leu Ser Leu Glu Glu Pro Gly Ser Pro Gly Gly Trp Arg Ser Gly
 68 145 150 155 160
 71 Arg Arg Arg Leu Asn Ser Ser Ser Gly Ser Gly Gly Ser Ser Ser
 72 165 170 175
 75 Ser Asn Ser Ser Ser Ser Gly Val Gly Ser Pro Ser Trp Ala Gly
 76 180 185 190

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79 Arg Leu Arg Gly Asp Ala Gln Gln Val Val Ala Ala Arg Ile Leu Ser
 80 195 200 205
 83 Pro Pro Gly Pro Glu Glu Ala Gln Arg Lys Leu Arg Ile Leu Gln Arg
 84 210 215 220
 87 Glu Leu Gln Asn Val Gln Val Asn Gln Lys Val Gly Met Phe Glu Ala
 88 225 230 235 240
 91 Gln Ile Gln Ala Gln Ser Ser Ala Ile Gln Ala Pro Arg Ser Pro Arg
 92 245 250 255
 95 Leu Gly Arg Ala Arg Ser Pro Ser Pro Cys Pro Phe Arg Ser Ser Ser
 96 260 265 270
 99 Gln Pro Pro Glu Arg Val Leu Ala Pro Cys Ser Pro Ser Glu Glu Arg
 100 275 280 285
 103 Arg Thr Lys Ser Trp Gly Glu Gln Cys Thr Glu Thr Pro Asp Thr Asn
 104 290 295 300
 107 Ser Gly Arg Arg Ser Arg Leu Ser Thr His Pro Ser Lys Asp Lys Glu
 108 305 310 315 320
 111 Gly Val Ala Pro Leu Leu Gly Pro Ala Ser Pro Thr Arg Leu Gly Thr
 112 325 330 335
 115 Gln Ser Pro Ser Thr Ser Val Arg Met Glu Arg Gly Thr Pro Ala Ser
 116 340 345 350
 119 Pro Arg Cys Gly Ser Pro Thr Pro Met Glu Thr Asp Lys Arg Val Ala
 120 355 360 365
 123 Pro Ser Leu Glu Arg Phe Gly Thr Ser Leu Thr Leu Ala Thr Lys Val
 124 370 375 380
 127 Ala Ala Ser Ala Ala Ser Ala Gly Pro His Pro Gly His Asp Ser Ala
 128 385 390 395 400
 131 Leu Met Glu Thr Gly Cys Glu Leu Gly Gly Met Arg Pro Trp Glu Ala
 132 405 410 415
 135 Gln Met Glu Arg Arg Gly Gln Phe Leu Gly Lys Glu Thr Gly Ser Thr
 136 420 425 430
 139 Pro Glu Pro Val Arg Thr His Met Arg Glu Pro Pro Gly Arg Val Gly
 140 435 440 445
 143 Arg Gly Ile His Ser Val Gly Gly Gln Gly Ser Trp Thr Pro Glu Val
 144 450 455 460
 147 Ile Lys Arg Pro Glu Glu Arg Ala Val Thr Ala Gln Ser Ser Glu Pro
 148 465 470 475 480
 151 Ser Glu Asp Pro Arg Trp Ser Arg Leu Pro Val Asp Leu Asp Ser Val
 152 485 490 495
 155 Gly Pro Glu Lys Gly Gly Asn Arg Ile Pro Gly Met Arg Gly Pro Gln
 156 500 505 510
 159 Gln Thr Leu Asp Ser Glu Arg Glu Gly Ser Pro Ala Leu Gly Leu Leu
 160 515 520 525
 163 Gly Gly Ser Gln Ala Ala Gln Pro Gly Ala Arg Gly Val Glu Glu Asp
 164 530 535 540
 167 Val His Tyr Gly Arg Met Leu Glu Pro Leu Pro Pro Gly Glu Val Thr
 168 545 550 555 560
 171 Thr Lys Leu Lys Glu Pro Gln Cys Leu Pro Gly Asp Arg Met Gly Met
 172 565 570 575
 175 Gln Pro Glu Ser Ser Ile Val Trp Pro Ser Ala Leu Glu Glu Ala Pro

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176	580	585	590
179	Leu Ile Trp Thr Arg Asp Thr Gly Val Gln Ser Lys Gly Thr Trp Gly		
180	595	600	605
183	Ser Gln Leu Pro Asp Gly Asp Ala His Pro Ser Cys Gln Glu Met Pro		
184	610	615	620
187	Pro Asp Gln Lys Asp Lys Ala Ser Leu Lys Glu Ala Cys Ser Pro Ser		
188	625	630	635
191	Asn Ile Pro Ala Ile Pro Ala Val Ile Ile Thr Asp Met Gly Ala Gln		
192	645	650	655
195	Glu Asp Gly Gly Leu Glu Glu Ile Gln Gly Ser Pro Arg Gly Pro Leu		
196	660	665	670
199	Pro Leu Arg Lys Leu Ser Ser Ser Ala Ser Ser Thr Gly Phe Ser		
200	675	680	685
203	Ser Ser Tyr Asp Asp Ser Glu Glu Asp Ile Ser Ser Asp Pro Glu Arg		
204	690	695	700
207	Thr Leu Asp Pro Asn Ser Ala Phe Leu His Thr Leu Asp Gln Gln Lys		
208	705	710	715
211	720	725	730
212	735	740	745
215	750	755	760
216	765	770	775
219	780	785	790
220	795	800	805
223	810	815	820
224	825	830	835
227	840	845	850
228	855	860	865
231	870	875	880
232	890	895	895
235	900	905	910
236	920	925	925
239	930	935	940
240	940	945	950
243	955	960	965
244	970	975	970
247	975	980	985
248	990	995	995
251	995	995	995
252	995	995	995
255	995	995	995
256	995	995	995
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275	Phe	Gly	Lys	Thr	Thr	Pro	Leu	Pro	Glu	Gly	Gln	Thr	Leu	Gln	His	Asp
276	980						985						990			
279	Val	Pro	Trp	Gln	Glu	Gly	Asn	Arg	Glu	Asp	Gly	Tyr	Leu	Ser	Gly	Leu
280	995						1000						1005			
283	Asp	Asn	Leu	Ile	Asp	Ile	Leu		Thr	Glu	Met	Ser	Gln	Gly	Ser	Pro
284	1010						1015						1020			
287	Leu	Thr	Gly	His	Arg	His	Arg		Ala	Pro	Cys	His	Phe	Ala	Arg	His
288	1025						1030						1035			
291	Leu	Cys	Leu	Ser	Pro	Leu	Ser		Ser	Pro	Asn	Ser	Ser	Phe	Ser	Cys
292	1040						1045						1050			
295	Leu	Ser	Ala	Tyr	Leu	Glu	Gln		Ser	Leu	Pro	Ser	Ala	Leu	Gln	Asp
296	1055						1060						1065			
299	Thr	Leu	Glu	Lys	Lys	Lys	Arg		Phe	Phe	Phe	Ser	Arg	Ser	Leu	Leu
300	1070						1075						1080			
303	Pro	Arg	Pro	Pro	Thr	Gly	Leu		Gly	Gly	Gly	Val	Ser	His	Ala	Leu
304	1085						1090						1095			
307	Ile	Glu	Pro	Pro	Ser	Arg	Arg		Glu	Leu	His	Lys	Ala	Arg	Pro	His
308	1100						1105						1110			
311	Ile	Leu	Leu	His	Ser	Glu	Ser		Ala	Arg	Val	Gln	Lys	Ala	Val	Ser
312	1115						1120						1125			
315	Leu	Val	Ala	Ser	Leu	Glu	Arg		Leu	Ser	Leu	Pro	Leu	Gly	Asp	Thr
316	1130						1135						1140			
319	Ala	Pro	Leu	Pro	Glu	Asn	Ser		Gly	Pro	His	Trp	Leu	Pro	Val	Gly
320	1145						1150						1155			
323	Ala	Leu	Leu	Pro	Pro	Ser	Gly		Cys	His	Gln	Ala	Gln	Ser	His	Leu
324	1160						1165						1170			
327	Cys	Leu	Ser	Pro	Arg	Ala	Leu		Lys	Pro	Gly	Gln	Gly	Pro	Asp	Phe
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345	gtgctgagcc	ccggcagcgt	tttcagcccc	gggagaggcg	cctctttctt	cttcccccca								180		
347	gccgagtcgc	tgtccccccg	ggagccccgg	agccccgggg	gctggcggag	cggccggcgc								240		
349	aggctgaata	gtagcagcgg	cagtggcagc	ggcagcagcg	gcagtagcgt	gagcagccca								300		
351	agttggctg	gtcgctcg	aggggaccgg	cagcagggtg	tggcagccgg	taccctctcc								360		
353	ccgccaggggc	cgaggagggc	caagaggaag	ctgcggatct	tgcagcgcga	gttgcagaac								420		
355	gtgcaggtga	accagaaaagt	gggcatgttt	gaggcgcaca	tccagggcaca	gagctccgccc								480		
357	attcaagcgc	cccgcagccc	gcgtttggc	agggctcgct	cgcctccccc	gtgcccccttc								540		
359	cgcagcagca	gtcagccccc	tggaagggtc	ctgggttcagg	gcccggag	cgaggaacgg								600		
361	aggacaaaagt	cctgggggaa	gcaatgtcca	gagacttcag	gaaccgactc	cgggaggaaaa								660		
363	ggagggccca	gcctatgctc	ctcgaggtg	aagaaaggaa	tgccacctct	tcccggccgg								720		
365	gtgcggcccta	caggatcaga	ggctcagggt	ccatccgctt	ttgttaaggat	ggagaagggt								780		
367	atccctgcca	gtcccccgctg	tggctcaccc	acagctatgg	aaattgacaa	aaggggctct								840		

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369	cctaccccg gaaactcgag ctgcctagct ccctcattgg ggctgttcgg agctagctta	900
371	acgatggcca cggaaagtggc a诶cgagagtt acatccactg ggccacacccg tccacaggat	960
373	cttgccctca ctgagccgtc tggggagagcc cgtgagctg aggacctgca gcccccaagag	1020
375	gccctgggtgg agaggcaggc gcagtttctg ggcagtgaga caagcccagc cccagaaaagg	1080
377	ggcggggcccc gcgatggaga accccctggg aagatgggga aaggatatct gccctgtggc	1140
379	atgccccggct ctggggagcc tgaagtgggc aaaaggccag aggagacgac tgtgagcgtg	1200
381	caaagcgcag agtcctctga tgccctgagc tgggtccaggc tgcccaggc cctggcctcc	1260
383	gtagggccctg aggaggcccg aagtggggcc cccgtggcg gggggcgttg gcagctctcc	1320
385	gacagagtgg agggagggtc cccaaacgctg ggcttgcctg gggcagccc ctcagcacag	1380
387	ccggggaccg ggaatgtgga ggcgggaaatt cttctggca gaatgctgga gccttgcgg	1440
389	tgttggacg ctgcgaaaga tctgaaaagaa cctcagtgcc ctccctggga caggggtgggt	1500
391	gtgcagccctg ggaactccag gtttggcag ggcaccatgg agaaaagccgg tttggcttgg	1560
393	acgcgtggca caggggtgca atcagagggg acttgggaaa gccagcggca ggacagtgtat	1620
395	gccctcccaa gtccggagct gctaccccaa gatcaggaca agccttcct gaggaaggcc	1680
397	tgcagcccca gcaacataacc tgctgtcatc attacagaca tgggcacccca ggaggatggg	1740
399	gccttggagg agacgcaggc aagccctcg ggcacacctgc ccctgaggaa actgtcctct	1800
401	tcctccgcct cttccacggg cttctccctca tcctacgaag actcagagga ggacatctcc	1860
403	agtgaccctg agcgcaccct ggaccccaac tcagttttcc tgcataccct ggaccagcag	1920
405	aaaccttagag tgaccaaattc atggaggaag ataaaaaaaaca tgggtcactg gtctcccttc	1980
407	gtcatgtcct tcaagaagaa gtacccctgg atccagctgg caggacacgc agggagttc	2040
409	aaggcagctg ccaatggcag gatcctgaag aagcactgtg agtcagagca ggcgtgcctg	2100
411	gaccgctga tgggtggatgt gctgaggccc ttctgtacccctg cctaccatgg ggtatgtgggt	2160
413	aaggacgggg agcgcatacaa ccagatggac gacctgtgg cccacttcga ctgcctctgt	2220
415	gtgtatggact gcaagatggg aatcaggacc tacctggagg aggagctcac gaaggcccgg	2280
417	aagaagccca gcctgcggaa ggacatgtac cagaagatga tcgaggtgga ccccgaggcc	2340
419	cccaccgagg agaaaaaaagc acagcgggct gtgaccaagc cacggtacat gcagtggcgg	2400
421	gagaccatca gctccacggc caccctgggg ttctggatcg agggaaatcaa aaaagaagac	2460
423	ggcaccgtga accgggactt caagaagacc aaaacgaggc agcaggtcac cgaggccttc	2520
425	agagagttca ctaaaggaaa ccataacatc ctgatcgct atcgggaccg gctgaaggcc	2580
427	attcgaacca ctctagaagt ttctcccttc ttcaagtgcc acgaggtcat tggcagctcc	2640
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431	accacgcccc tgcctgaggg ccagaccctg cagcatgacg tccctggca ggaggggaaac	2760
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448	ctgagccccg gcagcgtctt cagccctggg agaggcgcct cttctcttt ccccccagca	180
450	gagtgcgtgt cgctggagga gcctgggagt gctgggggtt ggcgcagcgg ccgacggagg	240
452	ctgaatagta gcagcggtag cggaggtggc agcagcacca gcaacagcac cagcagcagt	300
454	ggcgtggca gtcccagttt ggctggccgc ctgcgagggg acgcgcagca ggtggcgg	360
456	acccgcattcc tctcccccacc tggggccggag gaggcccaga ggaagctgag gattctgcag	420
458	cgcgaattgc aaaatgtgca ggtgaaccag aaagtggca tggcggagc gcaaattccag	480
460	gcacagaccc ctgctattca agcgcacccga agccgcgtt tggtagggc tcgttgcggcc	540
462	tccctgttc cttccgaag cagcagccag cttcttgaaa ggttcttggc tccatgttcc	600

VERIFICATION SUMMARY

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